

CRF Errors Corrected by the STIC Systems Branch

OIRF #16

CRF Processing Date: 4/11/2001

Serial Number: 09/757,100B

ENTERED

Edited by: [Signature]
Verified by: [Signature] (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lastname at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 2 - corrected amino acid nos.

EXaminer: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

RAW SEQUENCE LISTING

DATE: 04/11/2001

PATENT APPLICATION: US/09/757,100B

TIME: 15:26:09

Input Set : A:\Isph-533.txt

Output Set: N:\CRF3\04112001\I757100B.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Monia, Brett P.
 4 Gaarde, William A.
 5 Nero, Pamela S.
 8 <120> TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
 9 Expression
 11 <130> FILE REFERENCE: ISPH-0533
 13 <140> CURRENT APPLICATION NUMBER: US/09/757,100B
 C--> 14 <141> CURRENT FILING DATE: 2001-03-15
 16 <150> PRIOR APPLICATION NUMBER: 09/377,310
 17 <151> PRIOR FILING DATE: 1999-08-19
 19 <150> PRIOR APPLICATION NUMBER: PCT/US00/18999
 20 <151> PRIOR FILING DATE: 2000-07-13
 22 <160> NUMBER OF SEQ ID NOS: 44
 24 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

337 <210> SEQ ID NO: 2
 338 <211> LENGTH: 1052
 339 <212> TYPE: PRT
 340 <213> ORGANISM: Homo sapiens
 342 <400> SEQUENCE: 2
 343 Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser
 344 1 5 10 15
 346 Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala
 347 20 25 30
 349 Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu
 350 35 40 45
 352 Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val
 353 50 55 60
 355 Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val
 356 65 70 75 80
 358 Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His
 359 85 90 95
 361 Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu
 362 100 105 110
 364 Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr
 365 115 120 125
 367 Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu
 368 130 135 140
 370 Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala
 371 145 150 155 160
 373 Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile
 374 165 170 175
 376 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser
 377 180 185 190

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379 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro
380      195      200      205
382 Lys Ser Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile
383      210      215      220
385 Gln Gln Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile
386 225      230      235      240
388 Leu Lys Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu
389      245      250      255
391 Cys Phe Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu
392      260      265      270
394 Ala Ile Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys
395      275      280      285
398 Asn Pro Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr
399      290      295      300
401 Ser Asn Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile
402 305      310      315      320
404 Ala Gly Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile
405      325      330      335
407 Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn
408      340      345      350
410 Gly Thr Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg
411      355      360      365
413 Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met
414      370      375      380
416 Arg Thr His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile
417 385      390      395      400
419 Ile Asp Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu
420      405      410      415
422 Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln
423      420      425      430
425 Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala
426      435      440      445
428 Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val
429      450      455      460
431 Arg Glu Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His
432 465      470      475      480
434 Pro His Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp
435      485      490      495
437 Ile Ile Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln
438      500      505      510
440 Val Arg Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr
441      515      520      525
443 Gln Leu Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His
444      530      535      540
446 Arg Asp Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val
447 545      550      555      560
449 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr
450      565      570      575
452 Tyr Lys Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu

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453          580          585          590
455 Ser Ile Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe
456          595          600          605
458 Gly Val Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln
459          610          615          620
461 Gly Val Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg
462 625          630          635          640
464 Leu Pro Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr
465          645          650          655
467 Lys Cys Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu
468          660          665          670
470 Lys Ala Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu
471          675          680          685
473 Glu Arg Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp
474          690          695          700
476 Ser Gly Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr
477 705          710          715          720
479 Pro Ser Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met
480          725          730          735
482 Val Gln Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly
483          740          745          750
485 Ile Thr Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu
486          755          760          765
488 Asp Gln Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp
489          770          775          780
491 Gln Pro Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly
492 785          790          795          800
494 Gln Val Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln
495          805          810          815
497 Gln Glu Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe
498          820          825          830
500 Leu Lys Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp
501          835          840          845
503 Gly Ser Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val
504          850          855          860
506 Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly
507 865          870          875          880
509 Ala Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp
510          885          890          895
512 Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro
513          900          905          910
515 Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val
516          915          920          925
518 Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro
519          930          935          940
521 Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala
522 945          950          955          960
524 Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro
525          965          970          975

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```

527 Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser
528          980          985          990
530 Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val
531          995          1000          1005
533 Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala
534          1010          1015          1020
536 His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln
E--> 537 1025/1025          1030          1035          1040
539 Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
540          1045          1050
1033 <210> SEQ ID NO: 44
1034 <211> LENGTH: 20
1035 <212> TYPE: DNA
1036 <213> ORGANISM: Artificial Sequence
1038 <220> FEATURE:
1039 <223> OTHER INFORMATION: control sequence
1041 <220> FEATURE:
1042 <221> NAME/KEY: unsure
1043 <222> LOCATION: (1)..(20)
1045 <400> SEQUENCE: 44
W--> 1046 nnnnnnnnnn nnnnnnnnnn
E--> 1050 17

```

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VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:537 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:1046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1050 M:254 E: No. of Bases conflict, LENGTH:Input:17 Counted:20 SEQ:44